

RAW SEQUENCE LISTING

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Application Serial Number: 10/511,362
Source: PCT
Date Processed by STIC: 10/24/04

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RAW SEQUENCE LISTING

DATE: 10/24/2004

PATENT APPLICATION: US/10/511,362

TIME: 08:53:38

Input Set : A:\Sequence Listing.txt

Output Set: N:\CRF4\10242004\J511362.raw

3 <110> APPLICANT: The Government of the United States of America as
 4 represented by the Secretary of the Department of Health and
 5 Human Services
 6 Blackshear, Perry J.
 7 Zeldin, Darryl C.
 8 Graves, Joan P.
 9 Stumpo, Deborah J.

11 <120> TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR DIAGNOSTICS AND THERAPEUTICS
 FOR

12 HYDORCEPHALUS

14 <130> FILE REFERENCE: 4239-64828-02

C--> 16 <140> CURRENT APPLICATION NUMBER: US/10/511,362

C--> 16 <141> CURRENT FILING DATE: 2004-10-14

16 <150> PRIOR APPLICATION NUMBER: 60/374,184

17 <151> PRIOR FILING DATE: 2002-04-19

19 <150> PRIOR APPLICATION NUMBER: 60/388,266

20 <151> PRIOR FILING DATE: 2002-06-13

22 <150> PRIOR APPLICATION NUMBER: PCT/US03/12348

23 <151> PRIOR FILING DATE: 2003-04-18

25 <160> NUMBER OF SEQ ID NOS: 39

27 <170> SOFTWARE: PatentIn version 3.2

29 <210> SEQ ID NO: 1

30 <211> LENGTH: 2188

31 <212> TYPE: DNA

32 <213> ORGANISM: Homo sapiens

35 <220> FEATURE:

36 <221> NAME/KEY: CDS

37 <222> LOCATION: (106)..(1797)

39 <400> SEQUENCE: 1

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 43 Met Ile Lys Arg
 44 1

46 aga gcc cac cct ggt gcg gga ggc gac agg acc agg cct cga cgg cgc 165
 47 Arg Ala His Pro Gly Ala Gly Gly Asp Arg Thr Arg Pro Arg Arg Arg
 48 5 10 15 20

50 cgt tcc act gag agc tgg att gaa aga tgt ctc aac gaa agt gaa aac 213
 51 Arg Ser Thr Glu Ser Trp Ile Glu Arg Cys Leu Asn Glu Ser Glu Asn
 52 25 30 35

54 aaa cgt tat tcc agc cac aca tct ctg ggg aat gtt tct aat gat gaa 261
 55 Lys Arg Tyr Ser Ser His Thr Ser Leu Gly Asn Val Ser Asn Asp Glu
 56 40 45 50

58 aat gag gaa aaa gaa aat aat aga gca tcc aag ccc cac tcc act cct 309
 59 Asn Glu Glu Lys Glu Asn Asn Arg Ala Ser Lys Pro His Ser Thr Pro

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60	55	60	65	
62	gct act ctg caa tgg ctg gag gag aac tat gag att gca gag ggg gtc	357		
63	Ala Thr Leu Gln Trp Leu Glu Glu Asn Tyr Glu Ile Ala Glu Gly Val			
64	70 75 80			
66	tgc atc cct cgc agt gcc ctc tat atg cat tac ctg gat ttc tgc gag	405		
67	Cys Ile Pro Arg Ser Ala Leu Tyr Met His Tyr Leu Asp Phe Cys Glu			
68	85 90 95 100			
70	aag aat gat acc caa cct gtc aat gct gcc agc ttt gga aag atc ata	453		
71	Lys Asn Asp Thr Gln Pro Val Asn Ala Ala Ser Phe Gly Lys Ile Ile			
72	105 110 115			
74	agg cag cag ttt cct cag tta acc acc aga aga ctc ggg acc cga gga	501		
75	Arg Gln Gln Phe Pro Gln Leu Thr Thr Arg Arg Leu Gly Thr Arg Gly			
76	120 125 130			
78	cag tca aag tac cat tac tat ggc att gca gtg aaa gaa agc tcc caa	549		
79	Gln Ser Lys Tyr His Tyr Tyr Gly Ile Ala Val Lys Glu Ser Ser Gln			
80	135 140 145			
82	tat tat gat gtg atg tat tcc aag aaa gga gct gcc tgg gtg agt gag	597		
83	Tyr Tyr Asp Val Met Tyr Ser Lys Lys Gly Ala Ala Trp Val Ser Glu			
84	150 155 160			
86	acg ggc aag aaa gaa gtg agc aaa cag aca gtg gca tat tca ccc cgg	645		
87	Thr Gly Lys Lys Glu Val Ser Lys Gln Thr Val Ala Tyr Ser Pro Arg			
88	165 170 175 180			
90	tcc aaa ctc gga aca ctg ctg cca gaa ttt ccc aat gtc aaa gat cta	693		
91	Ser Lys Leu Gly Thr Leu Leu Pro Glu Phe Pro Asn Val Lys Asp Leu			
92	185 190 195			
94	aat ctg cca gcc agc ctg cct gag gag aag gtt tct acc ttt att atg	741		
95	Asn Leu Pro Ala Ser Leu Pro Glu Glu Lys Val Ser Thr Phe Ile Met			
96	200 205 210			
98	atg tac aga aca cac tgt cag aga ata ctg gac act gta ata aga gcc	789		
99	Met Tyr Arg Thr His Cys Gln Arg Ile Leu Asp Thr Val Ile Arg Ala			
100	215 220 225			
102	aac ttt gat gag gtt caa agt ttc ctt ctg cac ttt tgg caa gga atg	837		
103	Asn Phe Asp Glu Val Gln Ser Phe Leu Leu His Phe Trp Gln Gly Met			
104	230 235 240			
106	ccg ccc cac atg ctg cct gtg ctg ggc tcc tcc acg gtg gtg aac att	885		
107	Pro Pro His Met Leu Pro Val Leu Gly Ser Ser Thr Val Val Asn Ile			
108	245 250 255 260			
110	gtc ggc gtg tgt gac tcc atc ctc tac aaa gct atc tcc ggg gtg ctg	933		
111	Val Gly Val Cys Asp Ser Ile Leu Tyr Lys Ala Ile Ser Gly Val Leu			
112	265 270 275			
114	atg ccc act gtg ctg cag gca tta cct gac agc tta act cag gtg att	981		
115	Met Pro Thr Val Leu Gln Ala Leu Pro Asp Ser Leu Thr Gln Val Ile			
116	280 285 290			
118	cga aag ttt gcc aag caa ctg gat gag tgg cta aaa gtg gct ctc cac	1029		
119	Arg Lys Phe Ala Lys Gln Leu Asp Glu Trp Leu Lys Val Ala Leu His			
120	295 300 305			
122	gac ctc cca gaa aac ttg cga aac atc aag ttc gaa ttg tcg aga agg	1077		
123	Asp Leu Pro Glu Asn Leu Arg Asn Ile Lys Phe Glu Leu Ser Arg Arg			
124	310 315 320			

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126	ttc tcc caa att ctg aga cgg caa aca tca cta aat cat ctc tgc cag	1125
127	Phe Ser Gln Ile Leu Arg Arg Gln Thr Ser Leu Asn His Leu Cys Gln	
128	325 330 335 340	
130	gca tct cga aca gtg atc cac agt gca gac atc acg ttc caa atg ctg	1173
131	Ala Ser Arg Thr Val Ile His Ser Ala Asp Ile Thr Phe Gln Met Leu	
132	345 350 355	
134	gaa gac tgg agg aac gtg gac ctg aac agc atc acc aag caa acc ctt	1221
135	Glu Asp Trp Arg Asn Val Asp Leu Asn Ser Ile Thr Lys Gln Thr Leu	
136	360 365 370	
138	tac acc atg gaa gac tct cgc gat gag cac cgg aaa ctc atc acc caa	1269
139	Tyr Thr Met Glu Asp Ser Arg Asp Glu His Arg Lys Leu Ile Thr Gln	
140	375 380 385	
142	tta tat cag gag ttt gac cat ctc ttg gag gag cag tct ccc atc gag	1317
143	Leu Tyr Gln Glu Phe Asp His Leu Leu Glu Glu Gln Ser Pro Ile Glu	
144	390 395 400	
146	tcc tac att gag tgg ctg gat acc atg gtt gac cgc tgt gtt gtg aag	1365
147	Ser Tyr Ile Glu Trp Leu Asp Thr Met Val Asp Arg Cys Val Val Lys	
148	405 410 415 420	
150	gtg gct gcc aag aga caa ggg tcc ttg aag aaa gtg gcc cag cag ttc	1413
151	Val Ala Ala Lys Arg Gln Gly Ser Leu Lys Lys Val Ala Gln Gln Phe	
152	425 430 435	
154	ctc ttg atg tgg tcc tgt ttc ggc aca agg gtg atc cgg gac atg acc	1461
155	Leu Leu Met Trp Ser Cys Phe Gly Thr Arg Val Ile Arg Asp Met Thr	
156	440 445 450	
158	ttg cac agc gcc ccc agc ttc ggg tct ttt cac cta att cac tta atg	1509
159	Leu His Ser Ala Pro Ser Phe Gly Ser Phe His Leu Ile His Leu Met	
160	455 460 465	
162	ttt gat gac tac gtg ctc tac ctg tta gaa tct ctg cac tgt cag gag	1557
163	Phe Asp Asp Tyr Val Leu Tyr Leu Leu Glu Ser Leu His Cys Gln Glu	
164	470 475 480	
166	cgg gcc aat gag ctc atg cga gcc atg aag gga gaa gga agc act gca	1605
167	Arg Ala Asn Glu Leu Met Arg Ala Met Lys Gly Glu Gly Ser Thr Ala	
168	485 490 495 500	
170	gaa gtc cga gaa gag atc atc ttg aca gag gct gcc gca cca acc cct	1653
171	Glu Val Arg Glu Glu Ile Ile Leu Thr Glu Ala Ala Ala Pro Thr Pro	
172	505 510 515	
174	tca cca gtg cca tcg ttt tct cca gca aaa tct gcc aca tct gtg gaa	1701
175	Ser Pro Val Pro Ser Phe Ser Pro Ala Lys Ser Ala Thr Ser Val Glu	
176	520 525 530	
178	gtg cca cct ccc tct tcc cct gtt agc aat cct tcc cct gag tac act	1749
179	Val Pro Pro Pro Ser Ser Pro Val Ser Asn Pro Ser Pro Glu Tyr Thr	
180	535 540 545	
182	ggc ctc agc act aca ggt aat gga aag tcc ttc aaa aac ttt ggg tag	1797
183	Gly Leu Ser Thr Thr Gly Asn Gly Lys Ser Phe Lys Asn Phe Gly	
184	550 555 560	
186	ttaatgtttg aagaaagggc tttctgccag cctgggcaac atagtggagac ttcatttcca	1857
188	cacacacaaa aagccagaca tcttggtctca cacctgtagt cccagctact tgggaggctg	1917
190	aggtgggaga attgcttgag cccaggagct acgatcgac cactgcattc tagccttagt	1977
192	gatacagtga gaccttgtct caaaaaaaga aaaacagggc tttctggaaa aacattcttc	2037

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202 <211> LENGTH: 563
203 <212> TYPE: PRT
204 <213> ORGANISM: Homo sapiens
206 <400> SEQUENCE: 2
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209 1 5 10 15
212 Pro Arg Arg Arg Arg Ser Thr Glu Ser Trp Ile Glu Arg Cys Leu Asn
213 20 25 30
216 Glu Ser Glu Asn Lys Arg Tyr Ser Ser His Thr Ser Leu Gly Asn Val
217 35 40 45
220 Ser Asn Asp Glu Asn Glu Glu Lys Glu Asn Asn Arg Ala Ser Lys Pro
221 50 55 60
224 His Ser Thr Pro Ala Thr Leu Gln Trp Leu Glu Glu Asn Tyr Glu Ile
225 65 70 75 80
228 Ala Glu Gly Val Cys Ile Pro Arg Ser Ala Leu Tyr Met His Tyr Leu
229 85 90 95
232 Asp Phe Cys Glu Lys Asn Asp Thr Gln Pro Val Asn Ala Ala Ser Phe
233 100 105 110
236 Gly Lys Ile Ile Arg Gln Gln Phe Pro Gln Leu Thr Thr Arg Arg Leu
237 115 120 125
240 Gly Thr Arg Gly Gln Ser Lys Tyr His Tyr Tyr Gly Ile Ala Val Lys
241 130 135 140
244 Glu Ser Ser Gln Tyr Tyr Asp Val Met Tyr Ser Lys Lys Gly Ala Ala
245 145 150 155 160
248 Trp Val Ser Glu Thr Gly Lys Lys Glu Val Ser Lys Gln Thr Val Ala
249 165 170 175
252 Tyr Ser Pro Arg Ser Lys Leu Gly Thr Leu Leu Pro Glu Phe Pro Asn
253 180 185 190
256 Val Lys Asp Leu Asn Leu Pro Ala Ser Leu Pro Glu Glu Lys Val Ser
257 195 200 205
260 Thr Phe Ile Met Met Tyr Arg Thr His Cys Gln Arg Ile Leu Asp Thr
261 210 215 220
264 Val Ile Arg Ala Asn Phe Asp Glu Val Gln Ser Phe Leu Leu His Phe
265 225 230 235 240
268 Trp Gln Gly Met Pro Pro His Met Leu Pro Val Leu Gly Ser Ser Thr
269 245 250 255
272 Val Val Asn Ile Val Gly Val Cys Asp Ser Ile Leu Tyr Lys Ala Ile
273 260 265 270
276 Ser Gly Val Leu Met Pro Thr Val Leu Gln Ala Leu Pro Asp Ser Leu
277 275 280 285
280 Thr Gln Val Ile Arg Lys Phe Ala Lys Gln Leu Asp Glu Trp Leu Lys
281 290 295 300
284 Val Ala Leu His Asp Leu Pro Glu Asn Leu Arg Asn Ile Lys Phe Glu
285 305 310 315 320
288 Leu Ser Arg Arg Phe Ser Gln Ile Leu Arg Arg Gln Thr Ser Leu Asn

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289          325          330          335
292 His Leu Cys Gln Ala Ser Arg Thr Val Ile His Ser Ala Asp Ile Thr
293          340          345          350
296 Phe Gln Met Leu Glu Asp Trp Arg Asn Val Asp Leu Asn Ser Ile Thr
297          355          360          365
300 Lys Gln Thr Leu Tyr Thr Met Glu Asp Ser Arg Asp Glu His Arg Lys
301          370          375          380
304 Leu Ile Thr Gln Leu Tyr Gln Glu Phe Asp His Leu Leu Glu Glu Gln
305 385          390          395          400
308 Ser Pro Ile Glu Ser Tyr Ile Glu Trp Leu Asp Thr Met Val Asp Arg
309          405          410          415
312 Cys Val Val Lys Val Ala Ala Lys Arg Gln Gly Ser Leu Lys Lys Val
313          420          425          430
316 Ala Gln Gln Phe Leu Leu Met Trp Ser Cys Phe Gly Thr Arg Val Ile
317          435          440          445
320 Arg Asp Met Thr Leu His Ser Ala Pro Ser Phe Gly Ser Phe His Leu
321          450          455          460
324 Ile His Leu Met Phe Asp Asp Tyr Val Leu Tyr Leu Leu Glu Ser Leu
325 465          470          475          480
328 His Cys Gln Glu Arg Ala Asn Glu Leu Met Arg Ala Met Lys Gly Glu
329          485          490          495
332 Gly Ser Thr Ala Glu Val Arg Glu Glu Ile Ile Leu Thr Glu Ala Ala
333          500          505          510
336 Ala Pro Thr Pro Ser Pro Val Pro Ser Phe Ser Pro Ala Lys Ser Ala
337          515          520          525
340 Thr Ser Val Glu Val Pro Pro Pro Ser Ser Pro Val Ser Asn Pro Ser
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345 545          550          555          560
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353 <211> LENGTH: 3382
354 <212> TYPE: DNA
355 <213> ORGANISM: Homo sapiens
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360 <222> LOCATION: (110)..(2035)
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365 agacttcgct cagcaciaaag aagaattttc tgataaccat actggcaaaa atg aac tgg      118
366                                     Met Asn Trp
367                                     1
369 gct gcc ttc gga ggg tct gaa ttc ttc atc cca gaa ggc att cag ata      166
370 Ala Ala Phe Gly Gly Ser Glu Phe Phe Ile Pro Glu Gly Ile Gln Ile
371 5          10          15
373 gat tcg aga tgc cca cta agc aga aat atc acg gaa tgg tac cat tac      214
374 Asp Ser Arg Cys Pro Leu Ser Arg Asn Ile Thr Glu Trp Tyr His Tyr
375 20          25          30          35
377 tat ggc att gca gtg aaa gaa agc tcc caa tat tat gat gtg atg tat      262

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VERIFICATION SUMMARY

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L:16 M:271 C: Current Filing Date differs, Replaced Current Filing Date